

WO 00/28057

PCT/US99/26478

SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company

<120> Plant Aminoacyl-tRNA Synthetases

<130> BB1270

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<150> 60/107,789

<151> 1998-November-10

<160> 22

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<210> 1

<211> 1178

<212> DNA

<213> Zea mays

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<212> PRT

<213> Zea mays

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Gly Leu Ile Lys Glu Ser Glu Gly Ala Arg Val Ile Phe Ile Gln Gly
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His Gln Ile Pro Leu Ile Val Val Lys Ser Asp Gly Gly Phe Asn Tyr
      35             40             45

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Ala Ser Thr Asp Leu Thr Ala Leu Trp Tyr Arg Leu Asn Val Glu Gln
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Ala Glu Trp Ile Ile Tyr Val Thr Asp Val Gly Gln Gln Gln His Phe
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Asp Met Val Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Asp Pro
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Ser Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val
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Arg Leu Val Glu Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu
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Leu Leu Gln Arg Leu Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp
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Glu Glu Leu Glu Gln Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys
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Tyr Ala Asp Leu Lys Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe
180 185 190

Glu Gln Met Leu Ser Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr
195 200 205

Ala His Ala Arg Ile Cys Ser Ile Ile Arg Lys Ser Asn Lys Asn Val
210 215 220

Glu Glu Leu Lys Met Ser Gly Ala Ile Ser Leu Asp His Pro Asp Glu
225 230 235 240

Arg Val Leu Gly Leu Tyr Leu Ile Arg Phe Ala Glu Val Val Glu Glu
245 250 255

Ala Cys Thr Asn Leu Leu Pro Asn Val Val Cys Glu Tyr Leu Tyr Asn
260 265 270

Leu Ser Glu Met Phe Thr Lys Phe Tyr Thr Asn Cys Gln Val Val Gly
275 280 285

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Leu

<210> 3
<211> 2019
<212> DNA
<213> Oryza sativa

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aataaaaaaa aataatgtaa aaaaaaaaaa aaaaaaaaaa 2019

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<211> 587
<212> PRT
<213> Oryza sativa

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Glu Val Ser Lys Pro Gly Phe Gly Asp Tyr Gln Cys Asn Asn Ala Met
35 40 45
Ser Val Phe Ser Arg Ile Arg Gly Ser Ala Thr Asn Phe Arg Asn Pro
50 55 60
Met Ala Val Gly Gln Ala Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile
65 70 75 80
Ile Glu Ser Ile Ser Val Ala Gly Pro Gly Tyr Ile Asn Ile Thr Leu
85 90 95

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Ser Ser Asn Trp Ile Ala Gln Arg Ile Gln Asp Met Leu Val Cys Gly
 100 105 110
 Ile Lys Thr Trp Ala Pro Ile Leu Pro Val Lys Arg Ala Val Leu Asp
 115 120 125
 Phe Ser Ser Pro Asn Ile Ala Lys Glu Met His Val Gly His Ile Arg
 130 135 140
 Ser Thr Ile Ile Gly Asp Thr Leu Ala His Met Phe Glu Phe Thr Asn
 145 150 155 160
 Val Glu Val Leu Arg Arg Asn His Val Gly Asp Trp Gly Thr Gln Phe
 165 170 175
 Gly Met Leu Ile Glu Phe Leu Phe Glu Gln Phe Pro Asp Trp Glu Asp
 180 185 190
 Val Gly Asn Gln Ala Val Gly Asp Leu Gln Ser Phe Tyr Lys Ala Ser
 195 200 205
 Lys Lys Arg Phe Asp Asp Asp Pro Asp Phe Lys Glu Arg Ala Arg Gln
 210 215 220
 Ala Val Val Arg Leu Gln Gly Gly Glu Asp Lys Tyr Arg Ala Ala Trp
 225 230 235 240
 Lys Lys Ile Cys Gln Ile Ser Arg Met Glu Phe Asp Leu Val Tyr Lys
 245 250 255
 Arg Leu Asn Val Lys Leu Glu Glu Lys Gly Glu Ser Phe Tyr Asn Pro
 260 265 270
 Tyr Ile Pro Pro Val Leu Glu Glu Leu Thr Asn Lys Gly Leu Ile Val
 275 280 285
 Glu Ser Lys Gly Ala Arg Val Ile Phe Val Glu Asp His Pro Leu Ile
 290 295 300
 Val Ile Lys Gln Asp Gly Gly Phe Asn Tyr Ala Ser Thr Asp Leu Ala
 305 310 315 320
 Ala Leu Trp Tyr Arg Leu Asn Val Glu Lys Ala Glu Trp Ile Ile Tyr
 325 330 335
 Val Thr Asp Val Gly Gln Gln Arg His Phe His Met Leu Phe Thr Ala
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 Ala Lys Met Ala Gly Trp Leu Pro Glu Gln Asn Gly Lys Lys Tyr Pro
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 Lys Ala Ser His Val Gly Phe Gly Leu Val Leu Gly Ser Asp Gly Lys
 370 375 380
 Arg Phe Arg Thr Arg Cys Ser Glu Val Val Arg Leu Val Asp Leu Leu
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 Asp Glu Ala Lys Ala Arg Ser Lys Ala Gln Leu Ile Lys Arg Phe Thr
 405 410 415

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Gly Asn Gly Gln Ile Ala Asp Trp Thr Asp Asp Glu Leu Asp Arg Thr
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 Ser Glu Ala Ile Gly Tyr Gly Ala Val Lys Tyr Ser Asp Leu Lys Asn
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 Asn Arg Leu Thr Asp Tyr Thr Phe Ser Phe Asp Gln Met Leu Ser Asp
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 Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala His Ala Arg Ile Cys
 465 470 475 480
 Ser Ile Ile Arg Lys Ala Ser Lys Asp Val Glu Lys Leu Lys Met Thr
 485 490 495
 Gly Ala Ile Thr Leu Gly His Pro Tyr Glu Arg Phe Leu Gly Leu His
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 Leu Ile Gln Phe Thr Glu Val Val Glu Gln Ala Cys Ala Asp Leu Gln
 515 520 525
 Pro His Arg Leu Cys Asp Tyr Leu Tyr Ser Leu Ser Leu Thr Phe Ser
 530 535 540
 Lys Phe Tyr Thr Asn Cys Gln Val Val Gly Ser Pro Glu Glu Thr Ser
 545 550 555 560
 Arg Leu Leu Leu Cys Glu Ala Thr Gly Ile Ile Met Arg Gln Cys Phe
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 His Leu Leu Gly Ile Thr Pro Val His Lys Leu
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 <211> 1123
 <212> DNA
 <213> Glycine max

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 gattgtatat gttacagata ttgggcagca acagcacttt gatatgctat ttaaggccta 180
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<210> 6
 <211> 288
 <212> PRT
 <213> Glycine max

<400> 6
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 35 40 45
 Gln His Phe Asp Met Leu Phe Lys Ala Tyr Arg Arg Ala Gly Trp Leu
 50 55 60
 Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly
 65 70 75 80
 Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Ser Ser Glu
 85 90 95
 Val Val Arg Leu Val Asp Leu Leu Asp Glu Ala Lys Arg Arg Cys Lys
 100 105 110
 Ile Ala Ile Leu Glu Arg Asp Thr Thr Lys Asp Trp Ser Glu Glu Glu
 115 120 125
 Ile Glu Lys Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala
 130 135 140
 Asp Leu Lys Ile Asn Arg Leu Thr Asn Tyr Thr Phe Asn Phe Asp Gln
 145 150 155 160
 Met Leu Asn Asp Lys Gly Asn Thr Ala Val Tyr Leu Leu Tyr Ala His
 165 170 175
 Ala Arg Ile Cys Ser Ile Ile Arg Lys Ser Gly Lys Asp Ile Glu Glu
 180 185 190
 Val Lys Arg Asn Gly Lys Ile Val Leu Asp His Glu Asp Glu Arg Ala
 195 200 205
 Leu Gly Leu His Leu Leu Gln Phe Pro Glu Val Phe Glu Glu Ala Cys
 210 215 220
 Thr Asn Leu Leu Pro Asn Phe Leu Cys Glu Tyr Leu Tyr Asn Leu Ala
 225 230 235 240
 Glu Ile Phe Thr Lys Lys Phe Tyr Ala Asn Cys Gln Val Val Gly Ser
 245 250 255
 Pro Glu Glu Thr Ser Arg Leu Leu Leu Cys Glu Ala Thr Val Thr Val
 260 265 270
 Met Arg His Cys Phe Tyr Leu Leu Gly Ile Glu His Val Tyr Arg Leu
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<210> 7
 <211> 1041
 <212> DNA
 <213> Triticum aestivum

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<210> 8
 <211> 240
 <212> PRT
 <213> Triticum aestivum

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 35 40 45
 Leu Gly Asp Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu
 50 55 60
 Leu Gln Arg Leu Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Glu
 65 70 75 80
 Glu Leu Glu Gln Thr Ser Lys Ala Val Gly Tyr Gly Ala Val Lys Tyr
 85 90 95
 Ala Asp Leu Lys Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Asp
 100 105 110
 Gln Met Leu Ser Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala
 115 120 125
 His Ala Arg Ile Cys Ser Ile Ile Arg Lys Ser Asn Met Asp Val Glu
 130 135 140
 Glu Leu Lys Val Ser Gly Asn Ile Ser Leu Ala His Pro Asp Glu Arg
 145 150 155 160

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 <211> 715
 <212> PFT
 <213> Zed mays

<400> 10

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 35 40 45

Leu His Gly Val Asn Pro Ile Ile Leu Tyr Ile Ala Arg Gly Ala Ser
 50 55 60

Ile Ala Ser Leu Ser Gly Lys Asn Asp Ile Glu Phe Gly His Val Val
 65 70 75 80

Glu Trp Leu Glu Tyr Ala Pro Thr Phe Leu Ser Gly Ser Glu Phe Glu
 85 90 95

Asn Ala Cys Leu Phe Val Asp Gly Phe Leu Ala Ser Arg Thr Phe Leu
 100 105 110

Val Gly His Gly Leu Thr Ile Ala Asp Ile Ala Val Trp Ser Asn Leu
 115 120 125

Ala Gly Ile Gly Gln Arg Trp Glu Ser Leu Arg Lys Ser Lys Lys Tyr
 130 135 140

Gln Asn Leu Val Arg Trp Phe Asn Ser Ile Asp Ser Glu Tyr Lys Glu
 145 150 155 160

Ala Leu Asn Glu Val Val Ala Ala Phe Val Gly Lys Arg Gly Ile Gly
 165 170 175

Lys Ser Pro Ala Pro Ser Leu Lys Glu Lys Val His Asp Ser Lys Asp
 180 185 190

Pro Ser Ala Pro Glu Val Asp Leu Pro Gly Ala Lys Val Gly Lys Val
 195 200 205

Cys Val Arg Phe Ala Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His
 210 215 220

Ala Lys Ala Ala Leu Leu Asn Lys Tyr Phe Ala Glu Arg Tyr Gln Gly
 225 230 235 240

Arg Leu Ile Val Arg Phe Asp Asp Thr Asn Pro Ser Lys Glu Ser Asn
 245 250 255

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Glu Phe Val Glu Asn Leu Leu Lys Asp Ile Glu Thr Leu Gly Ile Lys
 260 265 270
 Tyr Asp Ala Val Thr Tyr Thr Ser Asp Tyr Phe Pro Lys Leu Met Glu
 275 280 285
 Met Ala Glu Ser Leu Ile Lys Gln Gly Lys Ala Tyr Ile Asp Asp Thr
 290 295 300
 Pro Lys Glu Gln Met Arg Lys Glu Arg Met Asp Gly Ile Glu Ser Arg
 305 310 315 320
 Cys Arg Asn Asn Thr Val Glu Glu Asn Leu Ser Leu Trp Lys Glu Met
 325 330 335
 Val Asn Gly Thr Glu Arg Gly Met Gln Cys Cys Val Arg Gly Lys Leu
 340 345 350
 Asp Met Gln Asp Pro Asn Lys Ser Leu Arg Asp Pro Val Tyr Tyr Arg
 355 360 365
 Cys Asn Thr Asp Pro His His Arg Val Gly Ser Lys Tyr Lys Val Tyr
 370 375 380
 Pro Thr Tyr Asp Phe Ala Cys Pro Phe Val Asp Ala Leu Glu Gly Val
 385 390 395 400
 Thr His Ala Leu Arg Ser Ser Glu Tyr His Asp Arg Asn Ala Gln Tyr
 405 410 415
 Tyr Arg Ile Leu Gln Asp Met Gly Leu Arg Arg Val Glu Ile Tyr Glu
 420 425 430
 Phe Ser Arg Leu Asn Met Val Tyr Thr Leu Leu Ser Lys Arg Lys Leu
 435 440 445
 Leu Trp Phe Val Gln Asn Lys Lys Val Glu Asp Trp Thr Asp Pro Arg
 450 455 460
 Phe Pro Thr Val Gln Gly Ile Val Arg Arg Gly Leu Lys Val Glu Ala
 465 470 475 480
 Leu Ile Gln Phe Ile Leu Gln Gln Gly Ala Ser Lys Asn Leu Asn Leu
 485 490 495
 Met Glu Trp Asp Lys Leu Trp Thr Ile Asn Lys Lys Ile Ile Asp Pro
 500 505 510
 Val Cys Ala Arg His Thr Ala Val Leu Lys Asp Gln Arg Val Ile Phe
 515 520 525
 Thr Leu Thr Asn Gly Pro Glu Glu Pro Phe Val Arg Ile Leu Pro Arg
 530 535 540
 His Lys Lys Phe Glu Gly Ala Gly Lys Lys Ala Thr Thr Phe Ala Asn
 545 550 555 560
 Arg Ile Trp Leu Asp Tyr Ala Asp Ala Ala Ala Ile Asn Lys Gly Glu
 565 570 575

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Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Val Lys Glu Ile Lys
580 585 590

Val Glu Ser Gly Val Ile Thr Glu Leu Val Gly Glu Leu His Leu Glu
595 600 605

Gly Ser Val Lys Thr Thr Lys Leu Lys Ile Thr Trp Leu Ala Asp Ile
610 615 620

Glu Glu Leu Val Pro Leu Ser Leu Val Glu Phe Asp Tyr Leu Ile Ser
625 630 635 640

Lys Lys Lys Leu Glu Glu Asp Glu Asp Phe Leu Asp Asn Leu Asn Pro
645 650 655

Cys Thr Arg Arg Glu Ile Pro Ala Leu Gly Asp Ala Asn Met Arg Asn
660 665 670

Ile Lys Arg Gly Glu Ile Ile Gln Leu Glu Arg Lys Gly Tyr Tyr Arg
675 680 685

Cys Asp Ala Pro Phe Ile Arg Ser Ser Lys Pro Val Val Leu Phe Ala
690 695 700

Ile Pro Asp Gly Arg Gln Gln Ala Ser Leu Ser
705 710 715

<210> 11
<211> 1920
<212> DNA
<213> Oryza sativa

<220>
<221> unsure
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<222> (431)

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<210> 12
 <211> 555
 <212> PRT
 <213> Oryza sativa

<220>
 <221> UNSURE
 <222> (130)

<400> 12
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 His Leu Arg Arg Pro Ser Pro Ser Ala Pro Pro Pro Pro Arg Arg
 20 25 30
 His Arg Thr Ala Pro Ala Ala Arg Cys Gly Pro Val Arg Ala Val Ala
 35 40 45
 Asp Gly Asn Leu His Val Gly Gly Ala Arg Thr Ala His Phe Asn Tyr
 50 55 60
 Leu Phe Ala Arg Ser Lys Gly Gly Lys Phe Val Leu Arg Ile Glu Asp
 65 70 75 80
 Thr Asp Phe Glu Arg Ser Thr Lys Lys Ser Glu Glu Ala Val Leu Ser
 85 90 95
 Asp Leu Ala Trp Leu Gly Leu Asp Trp Asp Glu Gly Pro Asp Val Gly
 100 105 110
 Gly Glu Tyr Gly Pro Asp Arg Gln Ser Glu Arg Asn Ser Met Tyr Lys
 115 120 125
 Gln Xaa Ala Glu Lys Leu Met Glu Ser Gly Ala Val Tyr Gln Cys Phe
 130 135 140
 Tyr Ser Ser Glu Gly Leu Glu Gln Met Lys Glu Thr Ala Ser Arg Cys
 145 150 155 160
 Asn Leu Pro Pro Val Tyr Ile Gly Lys Trp Gly Thr Ala Ser Asp Ala
 165 170 175

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Glu Ile Gln Gln Glu Leu Glu Lys Gly Thr Pro Tyr Thr Tyr Arg Phe
 180 185 190
 Arg Val Pro Lys Glu Gly Ser Leu Lys Ile Asn Asp Leu Ile Arg Gly
 195 200 205
 Glu Val Ser Trp Asn Leu Asp Thr Leu Gly Asp Phe Val Ile Met Arg
 210 215 220
 Ser Asn Gly Gln Pro Val Tyr Asn Phe Cys Val Thr Val Asp Asp Ala
 225 230 235 240
 Thr Met Arg Ile Ser His Val Ile Arg Ala Glu Glu His Leu Pro Asn
 245 250 255
 Thr Leu Arg Gln Ala Leu Ile Tyr Lys Ala Leu Gly Phe Pro Met Pro
 260 265 270
 Ser Phe Ala His Val Ser Leu Ile Leu Ala Pro Asp Arg Ser Lys Leu
 275 280 285
 Ser Lys Arg His Gly Ala Thr Ser Val Gly Gln Tyr Lys Glu Met Gly
 290 295 300
 Tyr Leu Pro Gln Ala Met Val Asn Tyr Leu Ala Leu Leu Gly Trp Gly
 305 310 315 320
 Asp Gly Thr Glu Asn Glu Phe Phe Thr Ile Asp Asp Leu Val Glu Lys
 325 330 335
 Phe Thr Ile Asn Arg Val Asn Lys Ser Gly Ala Val Phe Asp Ala Val
 340 345 350
 Lys Leu Lys Trp Met Asn Gly Gln His Leu Arg Ser Phe Pro Pro Asp
 355 360 365
 Val Leu Ile Lys Ser Phe Glu Asp Arg Trp Lys Asp Thr Gly Ile Leu
 370 375 380
 Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu Leu Leu Lys
 385 390 395 400
 Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu Ser Asn Leu
 405 410 415
 Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu Ala Lys Ser
 420 425 430
 Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu Ile Ser Ala
 435 440 445
 Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly Arg Asp Gly
 450 455 460
 Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys Arg Lys Gly
 465 470 475 480
 Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly Lys Leu His
 485 490 495

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PCT/US99/26478

Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys Ala Gly Thr
500 505 510

Cys Gly Ala Val Thr Gln Gln Ser Gly Phe Val Asn Leu Asp Glu Arg
515 520 525

Phe Arg Ile Leu Lys Glu Val Glu Trp Glu Ser Leu Val Gln Glu Gln
530 535 540

Glu Ser Pro Ala Glu Thr Ala Val Pro Ala Ser
545 550 555

<210> 13
<211> 731
<212> DNA
<213> Glycine max

<400> 13
gcaaaacaaa acagagaaaa tggcgctggt gtgtggcggc atgccatggt cgaaggatgat 60
agttcctccc attttccacc actctcacac cctctgcacc ttcttcttcc aacgacgccg 120
tttctcaagt ctctgctctc tccgaacaac caccaccggt tcgcttctgt ttcgctcctt 180
ctcccaccgg aaacctccac gtcggcggtg cccgaacggc cctcttcaac tacttggtcg 240
caagggtccaa aggtgggaaa tttgtgctga gaattgagga cactgacttg gagagggtcca 300
caaggaggatc tgaggaggcc atgctcaaag atctttcttg gcttggactt gattgggatg 360
aagggcctgg tggtggaggg gattatggtc cttataggca gtctgatagg aattctttat 420
acaagcaatt tgcggataac ctacaccaat ccggtcatgt ttatcgctgc ttctgttcta 480
atgaggaact agagaaaatg aaggaggatg ctaaaactaaa gcaactgcct ccagtgtaca 540
caggtaaatg ggccagtgc acaaatgagg aagtagaaga agagctagca aaagggaactc 600
cttacctta ccggttccga gtccctaaag gaagtttaaa aattaatgat caaatacgag 660
gcgaagttag ttggaacttg gatacgcttg gagattttgt gataatgagg agtaatggtc 720
agcctgttta t 731

<210> 14
<211> 404
<212> PRT
<213> Glycine max

<400> 14
Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly
1 5 10 15
Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly
20 25 30
Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Ser Thr
35 40 45
Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu
50 55 60
Asp Trp Asp Glu Gly Pro Gly Val Gly Gly Asp Tyr Gly Pro Tyr Arg
65 70 75 80
Gln Ser Asp Arg Asn Ser Leu Tyr Lys Gln Phe Ala Asp Asn Leu His
85 90 95
Gln Ser Gly His Val Tyr Arg Cys Phe Cys Ser Asn Glu Glu Leu Glu
100 105 110

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Lys Met Lys Glu Asp Ala Lys Leu Lys Gln Leu Pro Pro Val Tyr Thr
 115 120 125
 Gly Lys Trp Ala Ser Ala Thr Asn Glu Glu Val Glu Glu Glu Leu Ala
 130 135 140
 Lys Gly Thr Pro Tyr Thr Tyr Arg Phe Arg Val Pro Lys Gly Ser Leu
 145 150 155 160
 Lys Ile Asn Asp Gln Ile Arg Gly Glu Val Ser Trp Asn Leu Asp Thr
 165 170 175
 Leu Gly Asp Phe Val Ile Met Arg Ser Asn Gly Gln Pro Val Tyr Asn
 180 185 190
 Phe Cys Val Thr Val Asp Asp Ala Thr Met Ala Ile Ser His Val Ile
 195 200 205
 Arg Ala Glu Glu His Leu Pro Asn Thr Leu Arg Gln Ala Leu Ile Tyr
 210 215 220
 Lys Ala Leu Gly Phe Pro Met Pro His Phe Ala His Val Ser Leu Ile
 225 230 235 240
 Leu Ala Pro Asp Arg Ser Lys Leu Ser Lys Arg His Gly Ala Thr Ser
 245 250 255
 Val Gly Gln Phe Arg Asp Met Gly Tyr Leu Pro Gln Ala Met Val Asn
 260 265 270
 Tyr Leu Ala Leu Leu Gly Trp Gly Asp Gly Thr Glu Asn Glu Phe Phe
 275 280 285
 Thr Leu Glu Gln Leu Val Glu Lys Phe Thr Ile Glu Arg Val Asn Lys
 290 295 300
 Ser Gly Ala Ile Phe Asp Ser Thr Lys Leu Arg Trp Met Asn Gly Gln
 305 310 315 320
 His Leu Arg Ser Leu Pro Ser Glu Glu Leu Asn Arg Ile Ile Gly Glu
 325 330 335
 Arg Trp Lys Asp Ala Gly Ile Ala Thr Glu Ser Gln Gly Ile Phe Ile
 340 345 350
 Gln Asp Ala Val Leu Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp
 355 360 365
 Ser Glu Lys Ala Leu Ser Ser Leu Leu Ser Tyr Pro Leu Tyr Glu Thr
 370 375 380
 Leu Ala Ser Ala Glu Gly Lys Pro Ile Leu Glu Asp Gly Val Ser Glu
 385 390 395 400
 Val Ala Lys Ser

<210> 15
 <211> 407

WO 00/28057

PCT/US99/26478

<212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (14)

<220>
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 <222> (150)

<220>
 <221> unsure
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<220>
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<220>
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 <222> (401)

<400> 15
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 gcaaggacgc gattcgcgcc gtcaccaaca gggaatcttc atcttggttc cctacgtacg 180
 gccctcttca attacctgat tgcaaaagct acacgcggtg aattcatcct acgcatagag 240
 gacacagatn agtcaaggac tggttcctggt gcgattgaaa aactctgcgc tgnnttgaga 300
 tggggggggt taaaaaggga taaaagggct ggtccccaat ngaccgcaan ngggcctttc 360
 aaaaatctca aaagactttt aangttataa aaaaaaacnc nccataa 407

<210> 16
 <211> 79
 <212> PRT
 <213> Triticum aestivum

<220>
 <221> UNSURE
 <222> (55)

<220>
 <221> UNSURE
 <222> (69)

<400> 16
 Lys Phe Gln Asn Ser Leu Ser Glu Arg Leu Pro Ala Arg Thr Arg Phe
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<210> 18
 <211> 495
 <212> PRT
 <213> Zea mays

<400> 18

Met Leu Leu Arg Asp His Val Thr Asn Gly Ser Thr Val Ala Ala Met
 1 5 10 15

Asn Ser Ala Ser Val Ala Glu Trp Ala Thr Ser Leu Ser Leu Leu Phe
 20 25 30

Asp Pro Lys Cys Pro Gly Leu Glu Ser Leu Val Glu Lys Val Lys Glu
 35 40 45

Ile Val Glu Ser Asn Glu Val Arg Arg Leu Pro Lys Ile Pro Lys Gly
 50 55 60

Thr Arg Asp Phe Gly Lys Glu Gln Met Ala Ile Arg Glu Arg Ala Phe
 65 70 75 80

Ser Ile Ile Thr Ser Val Phe Lys Met His Gly Ala Thr Ala Leu Asp
 85 90 95

Thr Pro Val Phe Glu Leu Arg Glu Thr Leu Met Gly Lys Tyr Gly Glu
 100 105 110

Asp Ser Lys Leu Ile Tyr Asp Leu Ala Asp Gln Gly Gly Glu Leu Cys
 115 120 125

Ser Leu Arg Tyr Asp Leu Thr Val Pro Phe Ala Arg Tyr Val Ala Met
 130 135 140

Asn Ser Ile Ser Ala Leu Lys Arg Tyr Gln Ile Ala Lys Val Tyr Arg
 145 150 155 160

Arg Asp Asn Pro Ser Lys Gly Arg Tyr Arg Glu Phe Tyr Gln Cys Asp
 165 170 175

Phe Asp Ile Ala Gly Val Tyr Glu Pro Met Glu Pro Asp Phe Glu Val
 180 185 190

Ile Lys Val Leu Thr Glu Leu Leu Asn Gln Leu Asp Ile Gly Thr Tyr
 195 200 205

Glu Ile Lys Leu Asn His Arg Lys Leu Leu Asp Gly Met Leu Glu Ile
 210 215 220

Cys Gly Val Pro Pro Gln Lys Phe Arg Thr Val Cys Ser Ser Ile Asp
 225 230 235 240

Lys Leu Asp Lys Gln Thr Phe Glu Gln Val Lys Lys Glu Leu Val Asp
 245 250 255

Glu Lys Gly Ile Ser Asn Glu Thr Ala Asp Glu Ile Gly Asn Leu Val
 260 265 270

Lys Thr Arg Gly Pro Pro Leu Glu Val Leu Met Glu Leu Arg Lys Glu
 275 280 285

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Gly Ser Lys Phe Met Asn Asn Val Gly Ser Val Ala Ala Leu Asn Glu
 290 295 300
 Leu Glu Ile Leu Phe Lys Ala Leu Asp Lys Ala Asn Ala Ile Ser Lys
 305 310 315 320
 Ile Thr Phe Asp Leu Ser Leu Ala Arg Gly Leu Asp Tyr Tyr Thr Gly
 325 330 335
 Val Ile Tyr Glu Ala Val Phe Lys Gly Ala Ala Gln Val Gly Ser Ile
 340 345 350
 Ala Ala Gly Gly Arg Tyr Asp Asn Leu Val Gly Met Phe Ser Gly Lys
 355 360 365
 Gln Ile Pro Ala Val Gly Val Ser Leu Gly Ile Glu Arg Val Phe Ala
 370 375 380
 Ile Met Glu Gln Gln Glu Lys Glu Arg Asn Glu Lys Ile Arg Pro Thr
 385 390 395 400
 Glu Thr Glu Val Leu Val Ser Ile Leu Gly Lys Asp Leu Thr Leu Ala
 405 410 415
 Ala Glu Leu Val Ser Glu Leu Trp Asn Ala Gly Ile Lys Ala Glu Phe
 420 425 430
 Lys Leu Thr Thr Arg Val Ala Asn His Ile Lys Tyr Ala Leu Gln Ser
 435 440 445
 Ser Ile Pro Trp Met Val Leu Val Gly Glu Ser Glu Leu Gln Lys Gly
 450 455 460
 Thr Val Lys Leu Lys Asp Val Glu Ala Asn Gln Glu Glu Glu Val Asp
 465 470 475 480
 Arg Lys Asp Phe Val Arg Glu Leu Lys Lys Arg Leu Ser Lys Ser
 485 490 495

<210> 19
 <211> 754
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (18)

<220>
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<220>
 <221> unsure
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<220>
 <221> unsure
 <222> (720)

WO 00/28057

PCT/US99/26478

<220>
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 <222> (740)

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 gtcgaaaagg tctgcaagaa gtattaaatt gttattcagt accagaaaat ttatttggca 180
 aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240
 tgaaagctgt tggctctatct caagaggctg tccaggagct attgcaagtc ctttctgtga 300
 agtcattgac cgagtttagaa gagagacttg ggagcagtg ggaagcagtt gctgatctga 360
 aacagctatt ctcccttget gaaaaaattg gttactctaa atggcttcaa tttgatgcat 420
 cagttgttcg aggtcttget tactacactg gcattgtatt tgagggtttt gaccgagaag 480
 gaaagctgcg agctatctgt ggtggtggtc gatatgatca tttgttctca acttttgggtg 540
 ctgatgacat tgctgcatgt ggttttggat ttggtgatgc aagtcatagt ggaattgctc 600
 aaaagagaan ggtctgttac cgggaaagctt aacttgcaaa tagatgacat tgtgtgtgcc 660
 ttggaccaaa gatcttcaag ggatgtgctg ctatggggcc caacaatctc agngaaaaan 720
 ggcaaattgt tgaagttggn tttgggaaaa caaa 754

<210> 20
 <211> 243
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (6)

<220>
 <221> UNSURE
 <222> (203)

<220>
 <221> UNSURE
 <222> (235)

<220>
 <221> UNSURE
 <222> (238)

<400> 20
 Asn Met Asp Ile Ile Xaa Val Pro Gly Val Met Ala Glu Ala Glu Leu
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 Ile Ala Ser Ile Val Thr Leu Phe Lys Arg Ile Gly Ile Thr Glu Ser
 20 25 30
 Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu
 35 40 45
 Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile
 50 55 60
 Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu
 65 70 75 80
 Lys Ala Val Gly Leu Ser Gln Glu Ala Val Gln Glu Leu Leu Gln Val
 85 90 95

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PCT/US99/26478

Leu Ser Val Lys Ser Leu Thr Glu Leu Glu Glu Arg Leu Gly Ser Ser
 100 105 110
 Gly Glu Ala Val Ala Asp Leu Lys Gln Leu Phe Ser Leu Ala Glu Lys
 115 120 125
 Ile Gly Tyr Ser Lys Trp Leu Gln Phe Asp Ala Ser Val Val Arg Gly
 130 135 140
 Leu Ala Tyr Tyr Thr Gly Ile Val Phe Glu Gly Phe Asp Arg Glu Gly
 145 150 155 160
 Lys Leu Arg Ala Ile Cys Gly Gly Gly Arg Tyr Asp His Leu Phe Ser
 165 170 175
 Thr Phe Gly Ala Asp Asp Ile Ala Ala Cys Gly Phe Gly Phe Gly Asp
 180 185 190
 Ala Ser His Ser Gly Ile Ala Gln Lys Arg Xaa Val Cys Tyr Arg Glu
 195 200 205
 Ala Leu Ala Asn Arg His Cys Val Cys Leu Gly Pro Lys Ile Phe Lys
 210 215 220
 Gly Cys Ala Ala Met Gly Pro Asn Asn Leu Xaa Glu Lys Xaa Gln Ile
 225 230 235 240
 Val Glu Val

<210> 21
 <211> 1164
 <212> DNA
 <213> Triticum aestivum

<400> 21
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 ggccgtgttg gatatgtact ccgtaccaca acacttgttt actcaagttt gtgttattgt 120
 tgacaagctg gggaaactga gtagggaaga aattgagaag gaattgattt caactgggct 180
 gtcattctgaa gcagtacagg gcatcattga agtgctctct ctcaagtcac tgtccaaact 240
 tgaagaggtg ctaggctcag gtgttgaagc cgttgctgac ttgaagaagc tcttctcgct 300
 tgctgagcaa tatggttatt ctgattggat ctgtttcgat gcatctgttg ttcgtggcct 360
 tgcatactac acagggattg tttttgaggc ttttgatagg gaaggggaac tgagagcgat 420
 ttgtggtggg gggaggtatg acaggctact gtcaacattt ggaactgaag atgtaccagc 480
 ctgtggcctt ggatttggag atgctgtcat agtggagctg ctgaaagaaa agggctcttt 540
 gcctgacctg ccacgtcaaa tagatgacat tgtgttccca ttggacgagg agcttgaggg 600
 gccagcatct agtgttgcat cctgtctgag gaagaagggc agatctgtag acctttaga 660
 agacaagcgt ctgaaatggg tgttcaaaca tgctgagagg ataaacgcta gcaggctgat 720
 cttggttggg aaatccgagt gggagcgagg catggtccgt gtgaagatac tatcaaccag 780
 agaagagttc gaggtcaagg cgggcgaatt gcagtagctg ttagctgac tggtcgattt 840
 gaaggtttga cttgtcccct ttcttcttct tgatcatctt caacactgta agttttgcaa 900
 ttcacgtcgt gtatacaaac aattaggtgg ctttgaatgc tattgccatc ttctttcgga 960
 tcattcacct tgcaacaaac aaagaaattg taggttttgc cattcaccaa catgtattga 1020
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 aaaaaaaaaa aaaaaaaaaa aaaa 1164

<210> 22
 <211> 271

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<212> PRT

<213> Triticum aestivum

<400> 22

Lys Leu Gly Ile Thr Ser Ser Asp Val Gly Ile Arg Leu Ser Ser Arg
 1 5 10 15

Lys Val Leu Gln Ala Val Leu Asp Met Tyr Ser Val Pro Gln His Leu
 20 25 30

Phe Thr Gln Val Cys Val Ile Val Asp Lys Leu Gly Lys Leu Ser Arg
 35 40 45

Glu Glu Ile Glu Lys Glu Leu Ile Ser Thr Gly Leu Ser Ser Glu Ala
 50 55 60

Val Gln Gly Ile Ile Glu Val Leu Ser Leu Lys Ser Leu Ser Lys Leu
 65 70 75 80

Glu Glu Val Leu Gly Ser Gly Val Glu Ala Val Ala Asp Leu Lys Lys
 85 90 95

Leu Phe Ser Leu Ala Glu Gln Tyr Gly Tyr Ser Asp Trp Ile Cys Phe
 100 105 110

Asp Ala Ser Val Val Arg Gly Leu Ala Tyr Tyr Thr Gly Ile Val Phe
 115 120 125

Glu Ala Phe Asp Arg Glu Gly Glu Leu Arg Ala Ile Cys Gly Gly Gly
 130 135 140

Arg Tyr Asp Arg Leu Leu Ser Thr Phe Gly Thr Glu Asp Val Pro Ala
 145 150 155 160

Cys Gly Phe Gly Phe Gly Asp Ala Val Ile Val Glu Leu Leu Lys Glu
 165 170 175

Lys Gly Leu Leu Pro Asp Leu Pro Arg Gln Ile Asp Asp Ile Val Phe
 180 185 190

Pro Leu Asp Glu Glu Leu Glu Gly Pro Ala Ser Ser Val Ala Ser Cys
 195 200 205

Leu Arg Lys Lys Gly Arg Ser Val Asp Leu Val Glu Asp Lys Arg Leu
 210 215 220

Lys Trp Val Phe Lys His Ala Glu Arg Ile Asn Ala Ser Arg Leu Ile
 225 230 235 240

Leu Val Gly Lys Ser Glu Trp Glu Arg Gly Met Val Arg Val Lys Ile
 245 250 255

Leu Ser Thr Arg Glu Glu Phe Glu Val Lys Ala Gly Glu Leu Gln
 260 265 270

<210> 23

<211> 913

<212> DNA

<213> Zea mays

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<220>
 <221> unsure
 <222> (486)

<220>
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 <222> (677)

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 <222> (851)

<220>
 <221> unsure
 <222> (889)

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 <221> unsure
 <222> (893)

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 <221> unsure
 <222> (910)

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 ttaagagtga tgggtggcttc aactatgcct caacagactt aactgctctt tggatcggc 180
 tcaatggtga gcaggcagag tggatcatat atgttacaga tgttggtcag cagcagcact 240
 ttgacatggt tttcagtgcg gcaaagatgg ccggttggtt cccagatcca agtgaaaaga 300
 agtttccgaa aacaagccat gttggatttg gtcttggtct tggttcaaga tggcaagcgg 360
 ttccgaaccc gcagtactga ggttggttga ttggtagagc tacttgatga ggctaaatct 420
 cggagcaaat cagaactact acaacggctc actgaaaatg gcaaaattgt tgactggacg 480
 gatgangaat tagagcaaac ttcagaggct gttggatatg gtgctgtgaa gtacgctgat 540
 ctaaaaaata acaggctcac taattacaca tttagttttg aacaaatgct gagcgataag 600
 ggaaataactg ctgtgtacct tcagtatgca catgctcgta tttgttccat tttcggaaa 660
 tccaacaaga acgtggnaga ctgaagagat ggagccattt ctctcgacca tccggattag 720
 cgctgttggg gctgtatctt anccgatttg cagagttggt gaagaggatc acgaactact 780
 ccaaatttgt gtgtgaatac tgtcaatcan ctgaaagtca caanatcata caactgcaag 840
 tgggtgggtcc ngaggaacac cgggtgtgctt gcaacgacgc gtttcacna agnctcaccg 900
 ctcggatacn cat 913

<210> 24
 <211> 221
 <212> PRT
 <213> Zea mays

WO 00/28057

PCT/US99/26478

<220>

<221> UNSURE

<222> (96)

<220>

<221> UNSURE

<222> (156)

<220>

<221> UNSURE

<222> (220)

<400> 24

Phe Tyr Asn Pro Tyr Ile Pro Gln Val Leu Glu Glu Leu Ser Asn Lys
 1 5 10 15

Gly Leu Ile Lys Glu Ser Glu Gly Ala Arg Val Ile Phe Ile Gln Gly
 20 25 30

His Gln Ile Pro Leu Ile Val Val Lys Ser Asp Gly Gly Phe Asn Tyr
 35 40 45

Ala Ser Thr Asp Leu Thr Ala Leu Trp Tyr Arg Leu Asn Val Glu Gln
 50 55 60

Ala Glu Trp Ile Ile Tyr Val Thr Asp Val Gly Gln Gln Gln His Phe
 65 70 75 80

Asp Met Val Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Asp Xaa
 85 90 95

Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Phe Leu
 100 105 110

Val Gln Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg
 115 120 125

Leu Val Glu Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu
 130 135 140

Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Xaa Glu Leu Glu Gln
 145 150 155 160

Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala Asp Leu Lys
 165 170 175

Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Glu Gln Met Leu Ser
 180 185 190

Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala His Ala Arg Ile
 195 200 205

Cys Ser Ile Ile Arg Lys Ser Asn Lys Asn Val Xaa Asp
 210 215 220

<210> 25

<211> 551

<212> DNA

<213> Oryza sp.

WO 00/28057

PCT/US99/26478

<220>
<221> unsure
<222> (274)

<220>
<221> unsure
<222> (391)

<220>
<221> unsure
<222> (398)

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<221> unsure
<222> (407)

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<400> 25
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 gggtttgggg attaccagtg caacaatgct atgagtgtat tttcaagaat aagaggatcc 180
 gcaacaaact tccgtaaccc catggcagtt gggcaggcaa ttgcaaataa cctccccag 240
 tcaaatatta tcgaatccat ctctgttgcc gganctgggt acattaacat aacgttatcc 300
 agcaattgga ttgcacagag gatacaaaga catgcttggt tgtgggaatc aaaacatggg 360
 gaacaatcct taacctgttt aagaaggcaa ntgctggntt tttcaanccc caataattgc 420
 aaaaagaana tgcaagttgg gcaataatna aggncaacaa taaatngggg natancccaa 480
 ctcaaaangg ttgnggntca caaaanggtt aanttctcn acgtaaacan gttgggaaac 540
 nggggnacac a 551

<210> 26
 <211> 68
 <212> PRT
 <213> Oryza sp.

<220>
 <221> UNSURE
 <222> (51)

<400> 26
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 1 5 10 15
 Arg Gly Ser Ala Thr Asn Phe Arg Asn Pro Met Ala Val Gly Gln Ala
 20 25 30
 Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile Ile Glu Ser Ile Ser Val
 35 40 45
 Ala Gly Xaa Gly Tyr Ile Asn Ile Thr Leu Ser Ser Asn Trp Ile Ala
 50 55 60
 Gln Arg Ile Gln
 65

<210> 27
 <211> 411

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<212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (18)

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 <221> unsure
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<400> 27
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 acaactgac tagcatcact ttggtatcgt ctaaatgaag aaaaacttga atggattgta 120
 tatgttacag atattgggca gcaacagcac tttgatatnc tattnaaggc ctataggcgt 180
 gcaggttggt taccaaagga tgagaatgct tatccaaaat gtactcatat aggttttggt 240
 cttgttcttg gggaagatgg aaaacgattt cggactcgca ncagtnangt tgttcgatta 300
 gttgattact tgatgaagct aaaangcgct gtaaaattgc cntcttgaaa cgtgatacaa 360
 ctaaaggatt ggnctgaagg aggagatcga gaaaacatcc gaagcagttg g 411

<210> 28
 <211> 115
 <212> PRT
 <213> Glycine max

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<220>
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 <221> UNSURE
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<220>
 <221> UNSURE
 <222> (109)

<400> 28
 Val Glu Gly Val Asp Xaa Pro Leu Ile Ala Val Xaa Arg Asp Gly Gly
 1 5 10 15
 Xaa Asn Tyr Phe Thr Thr Asp Leu Ala Ser Leu Trp Tyr Arg Leu Asn
 20 25 30
 Glu Glu Lys Leu Glu Trp Ile Val Tyr Val Thr Asp Ile Gly Gln Gln
 35 40 45
 Gln His Phe Asp Xaa Leu Xaa Lys Ala Tyr Arg Arg Ala Gly Trp Leu
 50 55 60
 Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly
 65 70 75 80
 Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Xaa Ser Xaa
 85 90 95
 Val Val Arg Leu Val Asp Tyr Leu Met Lys Leu Lys Xaa Ala Val Lys
 100 105 110
 Leu Pro Ser
 115

<210> 29
 <211> 565

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<212> DNA
<213> Triticum sp.

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 caaaaacgag tcatgttggg ttggccttg ttcttggagc agatggcaag cgcttccgaa 120
 ctctgtagtac tgaggttggt cggttgggaa gacctacttg atgaggctaa atctcgaagt 180
 aaatcaagaa cttctccaag cgtctcactg gaaaatggta aaattgttga ctggactgat 240
 gaaggaaacta agagcaaact tcaaaaggca gtaagatatg gcgctgtcaa agtatgcggg 300
 tctgaaaagaa taaccgactg actaattaca ctccaacttt gattcaagan ctaagtgaca 360
 agggaataac tgctgtcnac ttcaataagc caagcccgta cctccanca ttcnaaaacc 420
 caacatgggtg tnnaaaacta aaangatggg anattccncc tgccanccaa atagctgcct 480
 gggacgnact aacngtatgc aanatgttaa aaggatgaca acncttccaa tgtcngggng 540
 aaactatnac taccnaagta aaagt 565

<210> 30
 <211> 33
 <212> PRT
 <213> Triticum sp.

<400> 30
 Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val Leu
 1 5 10 15
 Gly Ala Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg
 20 25 30

Leu

<210> 31
 <211> 546
 <212> DNA
 <213> Oryza sp.

<220>
 <221> unsure
 <222> (448)

<220>
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<400> 31
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 cattctccag gagtctgaaa gtggttttgc taaagaagcg gctgagcttt tgaaggatgg 120
 catcgatttg atcactgatg ctgacgcagc cctttcaaac ctgttgctgt atccctcca 180

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tgctacatta agcagtgatg aagctaaatc tgtggtgcaa gacaagcttt ctgaggttgc 240
atcaggactc atttctgctt atgatagcgg tgaactttgt caagcactag ctgagggccg 300
tgatggttgg cagaagtggg tgaaaatttt tggcaaatca cttaaaagaa agggaaagtc 360
actctttatg ccgctccgtg tactgctgac tggcaagctt catgggcctg acatgggcgg 420
caccgtagtc ctcatacaca aagccggnac tgtggagcgg tcactcaaca atccggtttc 480
gtaaatctcg acgagaggtc agaatcctga angagtggag tggagtcact ggtacaggac 540
aagatc

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<210> 32
 <211> 147
 <212> PRT
 <213> Oryza sp.

<400> 32
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 1 5 10 15
 Gly Ile Leu Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu
 20 25 30
 Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu
 35 40 45
 Ser Asn Leu Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu
 50 55 60
 Ala Lys Ser Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu
 65 70 75 80
 Ile Ser Ala Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly
 85 90 95
 Arg Asp Gly Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys
 100 105 110
 Arg Lys Gly Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly
 115 120 125
 Lys Leu His Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys
 130 135 140
 Ala Gly Thr
 145

<210> 33
 <211> 524
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (386)

<220>
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 <222> (459)

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<220>
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 <222> (481)

<220>
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<220>
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 <222> (486)

<400> 33
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 accactctca caccctcgc accttcttct tccaacgacg ccgtttctca gtctctgtc 120
 tctccgaaca accaccacc gttcgcgttc gtttcgctcc ttctcccacc ggaaacctcc 180
 acgtcggcgg tgcccgaacg gccctcttca actacttggt cgcaaggtcc aaaggtggga 240
 aatttgtgct gagaattgag gacactgact tggagaggtc caagtaggga gtctgaggag 300
 gccatgctca aagatctttc ttggcttgga cttgattggg atgaagggcc tgggtgttg 360
 aggggattat ggtccttaaa aggcantctg agaaggaatt ccttatacaa acaatatgcc 420
 gngaaacta cacaaatccg ggcaagttta accgctgcnt tctggtccaa agagggaact 480
 nanagnaat gaaaggaggt tgctaaacta aagcaactgg cccc 524

<210> 34
 <211> 94
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (63)

<400> 34
 Gln Arg Arg Arg Phe Ser Val Ser Ala Leu Ser Glu Gln Pro Pro Pro
 1 5 10 15
 Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly
 20 25 30
 Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly
 35 40 45
 Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Xaa Ser
 50 55 60
 Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu
 65 70 75 80
 Asp Trp Asp Lys Gly Leu Gly Val Gly Gly Asp Tyr Gly Pro
 85 90

<210> 35
 <211> 506
 <212> DNA
 <213> Glycine max

<220>
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 <222> (18)

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<220>
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 <222> (483)

<220>
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 <222> (505)

<220>
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 <222> (506)

<400> 35
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 gtcgaaaggt tctgcaagaa gtattaaatt gttattcagt accagaaaat ttatttggca 180
 aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240
 tgaaagctgt tggctctatct caagaggctg tccaggagct attgcaagtc ctttctgtga 300
 agtcattgac cgagtttagaa gagagacttg ggagagtggg gaagcagttg ctgatctgaa 360
 acagtattct cccttgctga aaaaattggg tactctaaat ggttcaattt gatgatagtt 420
 gttcgaggctc ttgcttacta cactggcatt gatttgaggg tttgacgaga ggaagctgca 480
 gcntctgtgt gtgtcaatac attggn 506

<210> 36
 <211> 48
 <212> PRT
 <213> Glycine max

<400> 36
 Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu
 1 5 10 15

Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile
 20 25 30

Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu
 35 40 45

<210> 37
 <211> 577
 <212> DNA
 <213> Triticum sp.

<220>
 <221> unsure
 <222> (140)

<220>
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 <222> (370)

<220>
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<220>
 <221> unsure
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<400> 37
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 gtgttgata tgtactccgt accacaacac ttgtttactc aagtttgtgt tattgttgac 120
 aagctgggga aactgagtan ggaagaaatt gagaaggaat tgatttcaac tgggctgtca 180
 tctgaagcag tacaggggcat cattgaagtg ctctctctca agtcactgtc caaacttgaa 240
 gaggtgctag gctcaggtgt tgaagccgtt gctgacttga agaacctctt ctgccttgct 300
 gagcaatatg gttattctga ttggatctgt ttcgatgcat ctgttggtcg tggccttgca 360
 tactacacan gggattgttt ttgaggcttt tgatagggaa gggaaactga nancatttgt 420
 ggtggggggg aggtatgaca ggctacgtca acatttgga ctgaagatnt ccaccctgtg 480
 nctttggatt tggaatcctg tcanagtga ctcnnaaga aaggtctttn ctacctgcac 540
 tcaaataata nattgntcca ttgncaagac ttggggg 577

<210> 38
 <211> 46
 <212> PRT
 <213> Triticum sp.

<220>
 <221> UNSURE
 <222> (38)

<400> 38
 Ile Arg Leu Ser Ser Arg Lys Val Leu Gln Ala Val Leu Asp Met Tyr
 1 5 10 15

Ser Val Pro Gln His Leu Phe Thr Gln Val Cys Val Ile Val Asp Lys
 20 25 30

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Leu Gly Lys Leu Ser Xaa Glu Glu Ile Glu Lys Glu Leu Ile
35 40 45